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Figure 97

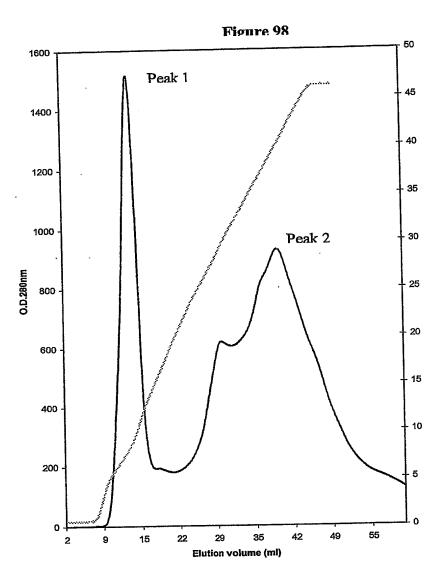
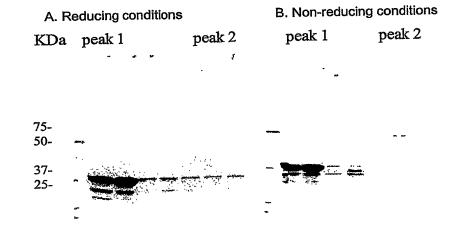
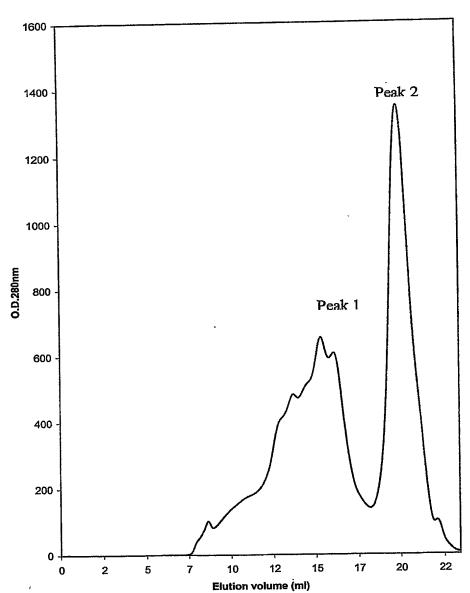


Figure 99



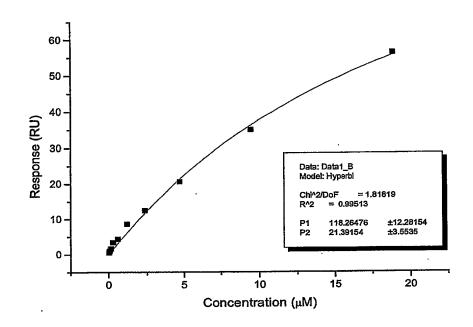
67/81 Figure 100



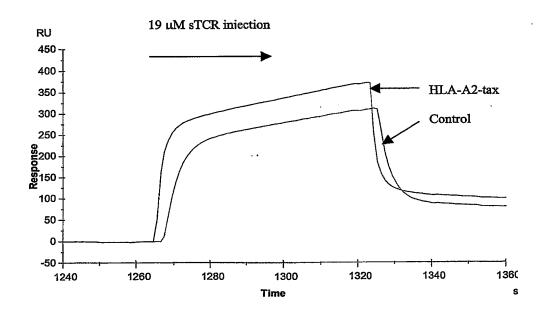
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Figure 101

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Figure 102

70/81 Figure 103

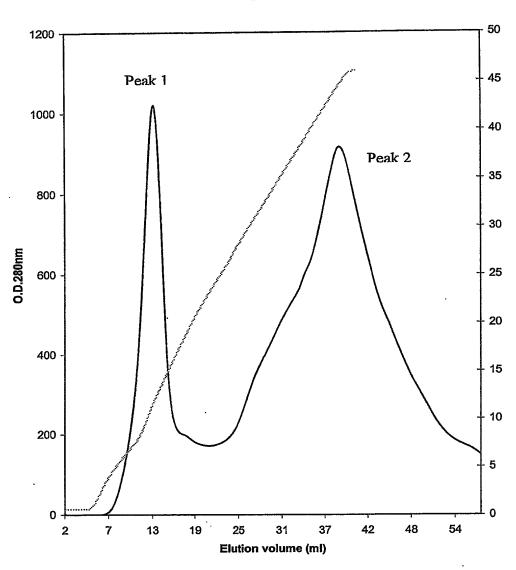
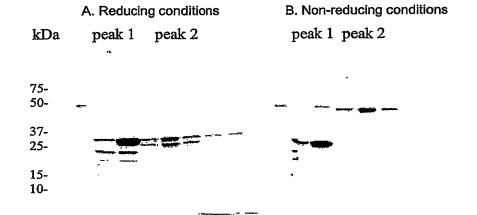
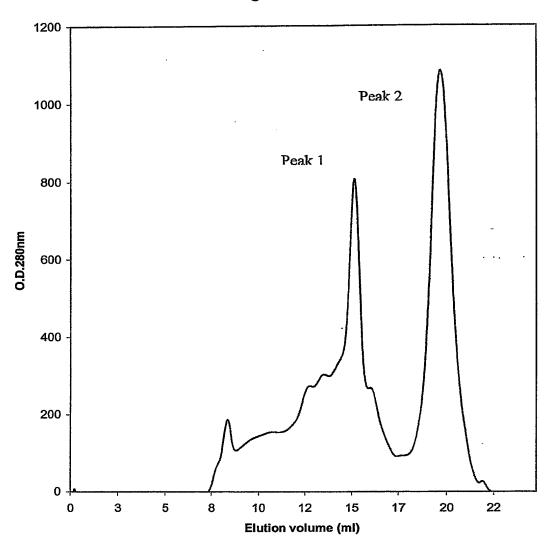


Figure 104

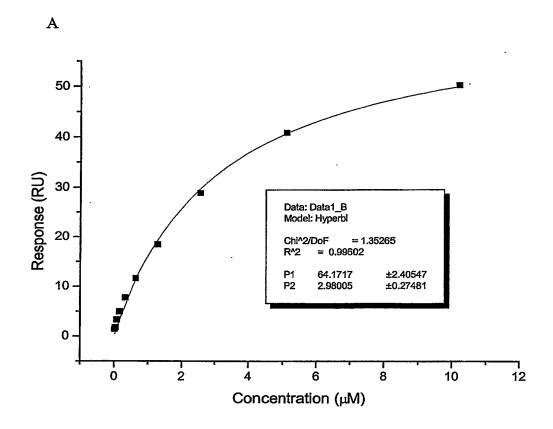


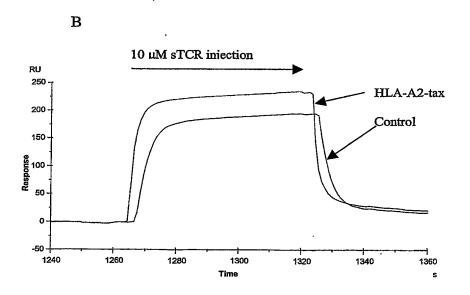
71/81 Figure 105



PCT/GB02/03986

72/81 Figure 106





CGTAGTTATC TACACGACGG GGAGICAGGC AACTAIGGAI GAACGAAATA GACAGAICGC IGAGAIAGGI GCCICACIGA ITAAGCAITG GIAACIGICA GACCAAGIII ACICAIAIAI GATTAAATAG AATTATTTT ATAGCACGTG ATGAAAAGGA CCCAGGTGGC ACTTTTCGGG AATAATATTG CATGAGTGAT ATATATCCAC GCGCCCTGAC AACGCGCGAG TAATACCIGA AACGCTGGTG CCCGAAGAAC TACACTATTC CTTGATCGTT CIGGCGAACI GTTTGTTGC CTICGITICC TGAATTGAAT CGCGCCTCGT GTAGAAGAGT AATTTCTTTT GACCCCAAAA GGCCGCATCT AATAATGTCA AACCAATCGT TATATTCTCC GCTAACAATA CCAATGTCAG AGCTCCAGCT GCGACGCGCC GIGGACICIT TGAGCTGALT CACACCGCAT GTCTGTGCTC AGCTAGCTAA TTICITICCL CAGCCCCGAC ACCCGCCAAC ACCCGCTGAC TGTGTCAGAG GTTTTCACCG TCATCACCGA TATTIGGATT TTAGAAGTA AATAAAGAAG TACATATATA TTTATTAGAC AAGAAAGCA CTACACAGAC AAGATGAAAC AATTCGGCAT TAAATGCTTC CTCACCCAGA GCTCGCCGCA TGTAACTCGC TGACACCACG AIGCCIGIAG CAAIGGCAAC AACGIIGCGC AAACIAITAA TTCCGGCTGG GGTGGTACGA ACATCCAATG AAGCACACAA TTTTTTTT CIGCCATAAC AAAGAAACCG AAATCAAAAA AAAGAATAAA AAAAAATGA GTAACTTACA GAGTTTTCGC GCTTCAAACC AAATCAGTCA TAGCTTTCGA CATGATTTAT CACTACATAT GCGTATATAT ACCAATCTAA TCTCGAGCTC TTTTTTTT GICTLIGICI GGCGAATGGC ACGGCACCTC TTCTTTATA GCTTAAAAAA TAGITITGCI TICCAACAAT TGTCATAATC CGCTCTTCGC AATGTCAACA GTACCCTTAG GACTGTATTA CCAACTTAAT CICCITICGC TGCGGTATTT TTTTTGCGGC ATTTTGCCTT CCTGTTTTTG GTTACATCGA ACTGGATCTC AACAGCGGTA AGATCCTTGA TIGGACAACA IGGGGGAICA GAGGCGGATA AAGTTGCAGG ACCACTTCTG CGCTCGGCCC TCALTGCAGC ACTGGGGCCA GATGGTAAGC CCTCCCGTAT ATGIAICCGC TCAIGAGACA AIAACCGIGA TCCCGTATTG ACGCCGGGCA AGAGCAACTC CTGGCGTTAC CTAGCGCCCG TTAGTGGTTT TCTGCCGCCT CCCGCAGAGT ACTGCAATTT CICCAICGAA TCGCTTGCCT TCTTCGGAAA ACAAAAACTA CATCTTACGG ATGGCATGAC AGTAAGAGAA TTATGCAGTG ACGCATGATA CAGCCTGAAT GGAGTCCACG TCGGCCTATT TACGCATCTG TACAGTTTTT TCCCTTTGCA AATAGTCCTC CCACACCGGG CGCCCTTCCC AACAGTTGCG ATTTTCTCCT TCGTTTTACA ACGTCGTGAC TGGGAAAACC GGGTTCCGAT TCATCTAAAC TTAGGACGGA GTGCCTGACT TGACTGACCG ATACATCCCT TGCCAGCGCC CITTGACGIT TTACTTATA TGTTACTTCT TAACTGTGCC TCCTTATATG TTTGCCGATT AACCGCTTTT TTATGTTTTG TCCGTATGAT GILLLICECC TATAAGGGAT CTGATGCGGT ATACATGCAT TAGCATCCCT GTCTCCCTTG AAATCTTTGT TCTGTATACA TTTAGCGGCT GTAATTCCTT AGCAGCACGT GTTTCTTCAA ATAGTTAAGC GGGAGCTGCA TAATGGTTTC AAGCGTACTT GTGTGGTCTT GTCTTTTACA CCGCTACACT GCTCCCTTTA TAGGIICCII CGAAGGAGCT CCGCACCGAT GCCGATAACA TGCTAACATC AAAAGGCCTC GCACACCGTG TGCALTCGTA ATGTCTGCCC ATTCTGCTAT GICTICGAAG AGTAAAAAT IGTACTIGGC GGATAAIGCC TAATGCTTCA ACTAACTCCA TGATATTAAA TAGCTTGGCA GCAACAGGAC TAGGATGAGT TCTTCCTTCT GTTCGGAGAT TACCGAATCA AAAAATTTC CTGATGCCGC GACCGTCTCC GTCATGATAA TTATTTTT TTTCAACAAA TCCCCTAGA TTTAAATTAT GAAAIGIGCG CGGAACCCCT AITIGITIAI IITITCIAAAI ACAIICAAAI CTTATTCCCT CGCGGTATTA CGCAGCGTGA TAAATCGGGG CTGATAGACG TTACAATTTC CCCTGTACCT GACCCAATGC GCAATTTCAT GGATTTTCGT GACCCGGGTA CTAGTATTAA TCTTTTGATT TGAGTTTAGT ATAGGTTAAT TACTCTGTGT TGCTATGTGG CACAGAAAAG ATCGGAGGAC GCTGAATGAA GCCATACCAA ACGACGAGCG GCTTCCCGGC AACAATTAAT AGACTGGATG TGAGCGTGGG TCTCGCGGTA CITACGCGTC GCGAAGAGGC CGTCAAGCTC GGCCATCGCC TITIAACAAA ATAIIAACGI GTAACGTTCA GAGCAATAAA AGTIGGGITA AGAATACIGG CACTCTCAGT ACAATCTGCT TCCGCTTACA GACAAGCTGT TACGGAATGA AGAAAAAAA ATAAACAAAG GTTTAAAAAA GATTAACGAT AAGTAAAATG TAAAATCACA GAGCAGGAAG AGCAAGATAA AAGGTAGTAT TTGTTGGCGA TITACITICI AITITIAAII TATAITITA TATIAAAAA CCGTGTCGCC GCACGAGTGG TCTCTTGTTC TTAATICAAT TCACTGGCCG GGTGGTTACG CTCTAATTTG CTATACTGTT CICGGICIAL TTTTGGGACC TTTGGGAATT TTCAACATTT AAAGTAAAAG ATGCTGAAGA TCAGTTGGGT ACTCACCAGT TCTGACAACG TCAACCCTAT ATGACAATTC GCCTATITIT TTTAAAGTTC GGCCCACAAG TCACGTAGTG TAAATTGAAG CIGCITITICI ATCCACGGTT TCTTCCACCC ATGTCTCTTT GTTTTTCCTT TGGCGTAATA CGGCGGGTGT CGGCTTTCCC TIGGLIGAGI CTGGAGCCGG TGTTCTGTGC AGTATGAGTA GATGAGCACT TGGATCCTAG AACAATGAAC TTTCGCCAGC CCACGITICGC GGAACAACAC TTAACGCGAA GCTTCCCAGC GAGCCCTTGC AGTAAACAAA GCICCCGGCA CTCGTGATAC GATGGAATAA CCAACTTACT TTAGTGAGGG GCATTAAGCG GGGTGATGGT CTGATATAT AGACCACATC TGGTATGGTG GGGAACCGGA ACTTACTCTA GCTGATAAAT AAAAAGGAAG GATCCTGTAG TGAAAAGCTG ATATACATTC PAATTCACCA CTGAATAAGG CTGTAGCGGC TCCTTTCTCG AACTTGATTA GTTCCAAACT TAACAAAAT AGGGTAATAA TCTCAAATAT AACCITCAIC AGTAGATAGG CCTGGCCCCA CAAATTTTCT ATGTGTTTTT TTTTCGTGCA TGCAGGTTTT CLTCCTTCGT GGGCTTGTCT ACGAAAGGGC ATCTTTTAAT GTTTTCCAAT TCAGAATGAC AACACTGCGG TTTGTTCCCT CACATCCCCC 401 501 601 701 801 901 1001 1101 1201 1301 1401 1501 1601 1701 1801 1901 2001 2101 2201 2301 2401 2501 2701 2801 3101 3201 3301 3401 3501 2601 2901 3001

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AGCTAGCTAA AGCTCCAGCT CGCCTTGCAG GCGACGCCC TTTCTTCCT GACCCCAAAA GTGGACTCTT	CACACCGCAT CATTACCTTG TTTAAATAAT TTGAACGCAC	TGCCTCATCC GTGGTGTGAT CTATACCTGT ACCAGCCTTT	ICCGCTAGGG SAAAGGACTG IGCACTCTCA ACTCGCTTA ACTTIGGGAA AAATAAACAA AAAAGGTAGT TTTATATATT TTTATATATT TATTCAACA GATCAGTTG CTTTTAAAGT GATCAGCAG GAACCATAC GGGGGGGGTG GGGGGGGGGG	5574
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Figure 108 continued

ACTTCATTTT CCCGTAGAAA TGCCGGATCA	CCACTTCAAG	GACTCAAGAC	GATACCTACA	GAGGGAGCTT	CGGAGCCTAT	CTGTGGATAA	CCCAATACGC	ATTAATGIGA	CAGGAAACAG	TGTCACGCTC	TICGGICCIC	AGATGCTTTT	GCGCCACATA	AACCCACTCG	AAGGGCGACA	GTATTTAGAA	AAATAGGCGT	ATGACAGAGT	TTATTCCAGA	GACGAATCCA	AACTTACTTA	GACGGTATCA	TGTTACACTC	ATACCACCTC	GCAGCAIARI TTTGTTTGTA	
ACTTCATTT CCCGTAGAAA TGCCGGATCA	CCACT	GACTO	GATAC	GAGGG	CGGAC	-						-		-	-		-	•	_		-		-	-		
TTGATTTAAA AGCGTCAGAC GTGGTTTGTT	AGTTAGGCCA	TACCGGGTTG	ACCGAACTGA	GAGAGCGCAC	GTCAGGGGG	TCCCCTGATT	CGGAAGAGCG	GCGCAACGCA	CAATTTCACA	GGCATCGTGG	CGGTTAGCTC	GCCATCCGTA	GGATAATACC	AGTTCGATGT	AAAAGGGAAT	ATATTTGAAT	TAACCTATAA	GCAGATGTAT	CACATGGTAT	GATGGAACTG	ACGGATATTT	AGACACTTCT	CCTCTATTGA	ATTCTCTCGG	AATATAAAGG TTTTCAATTT	
- •	-					-																				
ATACTTTAGA CGTTCCACTG GCTACCAGGG	GTGTAGCCGT	AGTCGTGTCT	AACGACCTAC	GICGGAACAG	TGTGATGCTC	TCCTGCGTTA	AGCGAGGAAG	CGGGCAGTGA	GAGCGGATAA	CGAGCTTGAT	TGAAAAAAG	TTACTGTCAT	CGTCAACACG	GTTGAGATCC	AATGCCGCAA	TGAGCGATAC	ATCATGACAT	GAGAAGTGCG	GICCIAGITA	GCGTAATGGT	TTTAAAGATT	CAATACATTC	TTTTCAGCTT	CAATCACACA	TGTAACAGGG	
-																			FTGTT	GGGA	TAGTG	BACCI	AAGAC	TAAAG	GCTCGGCTGC	! !
TTACTCATAT CGTGAGTTTT	TGTCCTTCTA	AGTGGCGATA	GCTTGGAGCG	AAGCGGCAGG	CGICGAITIT	ACATGTTCTT	CGAGICAGIG	GACTGGAAAG	GTGGAATTGT	GGCCGGCCGT	CCCCATGITG	CATAATTCTC	TCTTGCCCGG	TCTTACCGCT	AGGAAGGCAA	TATTGTCTCA	AACCATTATT	TTCCCTCATG	AGATGTTGTT	CCIPACGGGA	CTACATAGTG	GTGAGGACCT	GTTCTAAGAC	TTAATTAAAG	GCTCGGCTGC	1 1 1 1
		GGCTGCTGCC	ACACAGCCCA	GGTATCCGGT	CTGACTTGAG	CCTTTTGCTC	CCGAGCGCAG	CAGGTTTCCC	CCIAIGIIGI	TIGGGTACCG	TTACATGATC	GCAGGAACTG	ACCGAGTTGC	CTCTCAAGGA	GAGCAAAAAC	TTATCAGGGT	ACGTCTAAGA	CTTCTTCAGA	GAAGACCCAG	TACCAATGTT	GGAGACCTAA	GATTTAAACT	AAGATTACCC	TTCTCCGAAA	TATACCITIG	1) . 1
CAGACCAAGT AATCCCTTAA	TACCA	GGCTG		GGTAT	CTGAC	CCLTT	CCGAG	CAGGI	CCTAI	TIGGG	TTACA															
TGGTAACTGT TCATGACCAA AATCTGCTGC	AGAGCGCAGA	TGTTACCAGT	GGGTTCGTGC	AAGGCGGACA	TTCGCCACCT	CTTTTGCTGG	AGCCGAACGA	GCTGGCACGA	GCITCCGGCT	ATAGGGCGAA	TCAAGGCGAG	CATGGTTATG	GIATGCGGCG	GGGCGAAAA	GTTTCTGGGT	ATTGAAGCAT	GTGCCACCTG	TAIGGICALL	AGGCAAGAGA	TIGAAICGIT	TGATTGTGAG	GTGTGAGCGG	AGGITGGIGG	GCATGTGAGA	AAGGAGCCTA	Set Down
GATTAAGCAT TTTGATAATC TTCTGCCCT	IGGCTTCAGC	CTGCTAATCC	GCTGAACGGG	CGAAGGGAGA	CCTGTCGGGT	GGTTCCTGGC	CGCICGCCGC	CATTAATGCA	TACACTTTAT	ACGACTCACT	TTCCCAACGA	TGTTATCACT	TGAGAATAGT	AACGIICIIC	TTTCACCAGC	TTTCAATATT	TCCCCGAAAA	GGGATCTACG	CITCCAIGAT	TACGAAGAGT	CCAAATGGAC	TCCTACGTTA	GGAACCCATC	ATCTTCAGTG	TGCTAATGCA	AAAACACATA
-	_	_									-	_	_		_	-	-	_	_	_						
GIGCCICACI GAAGAICCII	GGAGGTAAC	ATACCTCGCT	CAGCGGTCGG	CCACGCTTCC	TCTTTATAGT	GCCTTTTTAC	GAGCTGATAC	TIGGCCGAIT	CCCCAGGCTT	AGCTCGAAAT	TCAGCTCCGG	TTGGCCGCAG	CAAGICATIC	ATCATTGGAA	CATCTTTAC	ACTCTTCCTT	CGCGCACATT	TCAAGAATTG	TATTCAGGCA	TAGATGGACA	ACCGTGCTAC	GTTATAATAA	ATTATATCTA	CCAGITITIA	TTGTTACGCA	ATAACTACAA
																									TGGT	ATCT
GCTGAGATAG GGATCTAGGT	ALCITTITC ACTCTTTTTC	CACCGCCTAC	GGATAAGGCG	TGAGAAAGCG	ACGCCTGGTA	CAGCAACGCG	GCCTTTGAGT	TCCCGGGGG	TCATTAGGCA	GATTACGCCA	ATGGCTTCAT	CAGAAGTAAG	TGTACTCAAC	AAAAGTGCTC	TGATCTTCAG	GAATACTCAT	ATAGGGTTC	CCTTTCGTCT	CAAGAGACTT	TGAAATGGTT	CGTCCTGAGG	ATTTTTGA	TCCCTTCGAG	TTTCTGGCAT	GACAGGTGGT	AGIGAACIIG GCTTAAATCT
GATC (TACC												TITC	CTGA	CATA	ATGCC	TTAT	CCCT	AAACT	TCLL
TAGACAGATC GCTGAGATAG TAATTTAAAA GGATCTAGGT	AGAICAAAGG	AACTCTGTAG	GATAGTTACC	GCGTGAGCTA	CCAGGGGGAA	GGAAAAACGC	CCGTATTACC	AAACCGCCTC	GTTACCTCAC	CTATGACCAT	GTCGTTTGGT	CGATCGTTGT	CTGTGACTGG	GCAGAACTTT	TGCACCCAAC	CGGAAATGTT	AAATAAACAA	ATCACGAGGC	CGCCAGTTTC	GTATTCCTGA	ТСААТАСАТА	GAATAATGCC	CCCTACTTAT	GGACACCCCT	GGTTGAAACT	TIAGGAGITI
3801 3901	4001 4101	4201	4301	4401	4501	4601	4701	4801	4901	5001	5101	5201	5301	5401	5501	5601	5707	5801	5901	6001	6101	6201	6301	6401	6501	6701

IleValHisPro TyrileGln AsnProAsp ProAlaValTyr GlnLeuArg AspSerLys SerSerAspLys SerValCys LeuPheThr AspPheAspSer LeuserValpro GludiyGlu AsnLeuVal LeuAsnCysser PheThrAsp SerAlaile TyrAsnLeuGin TrpPheArg GlnAspPro GlyLysGlyLeu MetArg Pheproser IlepheThr AlaValLeuPhe AlaAlaSer SerAlaLeu AlaAlaProVal AsnThrThr ThrGluAsp GluThrAlaGln ..Thrserkeu keukeulle Glnsersergin Argdudin Thrserdly ArgleuAsnAla serkeuAsp Lysserser GlyArgserThr keuTyrlle ..GlnThrAsn ValSerGln SerLysAspSer AspValTyr IleThrAsp LysCysValLeu AspMetArg SerMetAsp PheLysSerAsn SerAlaVal ..Ilebroala Glualaval IleglyTyrLeu Aspleuglu GlyaspPhe AspValalaval LeuProPhe Serasnser Thrasnashangur LeuLeuPhe GGCCTGGAGC AACAAATCTG ACTTTGCATG TGCAAACGCC TTCAACAACA GCATTATTCC AGAAGACACC TTCTTCCCCA GCCCAGAAAG TTCCTAACTC ATTGTTCATC CGTATATCCA GAACCCGGAT CCTGCCGTGT ACCAGCTGAG AGACTCTAAA TCCAGTGACA AGTCTGTCTG CCTATTCACC GATTTTGALT CTCAAACAAA TGTGTCACAA AGTAAGGATT CTGATGTGTA TATCACAGAC AAATGTGTGC TAGACATGAG GTCTATGGAC TTCAAGAGCA ACAGTGCTGT ·IleAsnThr ThrIleAlaSer IleAlaAla LysGluGlu GlyValSerLeu AspLysArg GluAlaGlu AlaGluGluVal ThrGlnIle ProAlaAla ThraAnnamy proceedings of the Company of the C TCACATCTCT GITGCTIATT CAGTCAAGTC AGAGAGGCA AACAAGTGGĀ AGĀCTTAATG CCTCGCTGGĀ TAAATCATCA GGĀCGTAGTA CTTTATACAT GlnbroglyAsp SerAlaThr TyrLeuCys AlaValArgPro ThrSerGly GlySerTyr IleProThrPhe GlyArgGly ThrSerLeu TGCAGCTICT CAGCCTGGTG ACTCAGCCAC CTACCTCTGT GCTGTGAGGC CCACATCAGG AGGAAGCTAC ATACCTACAT TTGGAAGAGG AACCAGCCTT CTGAGTGTCC CAGAAGGAGA AAACTTGGTT CTCAACTGCA GTTTCACTGA TAGCGCTATT TACAACCTCC AGTGGTTTAG GCAGGACCCT GGGAAAGGTC AlaTrpSer AsnLysSerAsp PheAlaCys AlaAsnAla PheAsnAsnSer IleIlePro GluAspThr PhePheProSer ProGluSer Ser*** A CHAIRT BANG TO THE CHAIRT BANG TO CARROLL CONTRACTOR .AlaAlaSer 801 901 101 201 301 401 501 601 701

The pre-pro mating factor alpha sequence is highlighted. BamHI site is underlined.

ValLeulysThr GlyGlnSer MetThrLeu GlnCysAlaGln AspMetAsn HisGluTyr MetSerTrpTyr ArgGlnAsp ProGlyMet GlyLeuArgLeu ValLeuGluAsp LeulysAsn ValPhePro ProGluValAla ValPheGlu ProSerGlu AlaGluIleSer HisThrGln LysAlaThr LeuValCysLeu Pheproser IlepheThr AlaValLeuPhe AlaAlaSer SerAlaLeu AlaAlaProVal AsnThrThr ThrGluAsp GluThrAlaGln ..AlaThrGly PheTyrPro AspHisValGlu LeuSerTrp TrpValAsn GlyLysGluVal HisSerGly ValCysThr AspProGlnPro LeuLysGlu ileglyTyrLeu AspLeuGlu GlyAspPhe AspValAlaVal LeuProPhe SerAsnSer ThrAsnAsnGly LeuLeuPhe ..11eHisTyr SerValGly AlaGlyIleThr AspGlnGly GluValPro AsnGlyTyrAsn ValSerArg SerThrThr GluAspPhePro LeuArgLeu GCAGCCCGCC CTCAATGACT CCAGATACGC TCTGAGCAGC CGCCTGAGGG TCTCGGCCAC CTTCTGGCAG GACCCCGCA ACCACTTCCG CTGTCAAGTC CAGTICTACG GGCTCTCGGA GAATGACGAG TGGACCCAGG ATAGGGCCAA ACCCGTCACC CAGATCGTCA GCGCCGAGGC CTGGGGTAGA GCAGACTAAC aaltiecegeorgangener argennam merminaer megenning mentre erenninge min hyegangan meneramak gennem meneram mene •Ileasnin Thriealaser ilealaala Lysglugiu Glyvalserieu Asplysang Glualagiu alagiyvalin Ginihrpro Lysphegin paraanken penameera ecamegnegungan araken erenning menerak keneragin menerak generakan menerakan cicagaccc aaan iccag GTACTGGAGG ACCTGAAAAA CGTGTTCCCA CCCGAGGTCG CTGTGTTTGA GCCATCAGAA GCAGAGATCT CCCACACCA AAAGGCCACA CTGGTGTGCC GICCIGAAGA CAGGACAGAG CAIGACACIG CAGIGIGCCC AGGAIAIGAA CCAIGAAIAC AIGICCIGGI AICGACAAGA CCCAGGCAIG GGGCIGAGGC TGATICATTA CICAGITGGI GCTGGIAICA CIGACCAAGG AGAAGICCCC AAIGGCIACA AIGICICCAG AICAACCACA GAGGATITCC CGCICAGGCI ·LeuSerAla AlaproserGln ThrSerVal TyrPheCys AlaSerSerTyr ValGlyAsn ThrGlyGlu LeuPhePheGly GluGlySer ArgLeuThr GCTGTCGGCT GCTCCCTCCC AGACATCTGT GTACTTCTGT GCCAGCAGTT ACGTCGGGAA CACCGGGGGAG CTGTTTTTG GAGAAGGCTC TAGGCTGACC Leudsnäspser ArgTyrala Leuserser ArgLeudrgval seralathr Phetrpgin AspProArgdsn HisPheArg CysGlnval GlnPheTyrGly LeuSerGlu AsnAspGlu TrpThrGlnAsp ArgAlaLys ProValThr GlnIleValSer AlaGluAla TrpGlyArg .IleProAla GluAlaVal GlnProAla 301 601 1001 401 501 701 801 101 201

The pre-pro mating factor alpha sequence is highlighted.

Figure 111



Figure 112

ggatccagcatggtgtgtctgaagctccctggaggctcctgcatgacagcgctgaca gtgacactgatggtgctgagctccccactggctttgtccggagacaccggtggcgga tctctagttccacgcggtagtggaggcggtggttccggagacacgcgttagtaggtc gacggaggcggtgggtagaatcgcccggctggaggaaaaagtgaaaaccttgaaa gctcagaactcggagctggcgtccacggccaacatgctcagggaacaggtggcacag cttaaacagaaagtcatgaactactaggatcc

Figure 113

BamHI		AgeI		Sal	I	BamHI
	DRβ Leader	GDT	TCR chain	Stop	Zipper	

ggatccagcatggtgtctgaagctccctggaggctcctgcatgacagcgctgaca gtgacactgatggtgctgagctccccactggctttgtccggagacaccggagacacc ggacagaaggaagtggagcagaactctggacccctcagtgttccagagggagccatt gcctctctcaactgcacttacagtgaccgaggttcccagtccttcttctggtacaga caatattctgggaaaagccctgagttgataatgtccatatactccaatggtgacaaa atcagagactcccagcccagtgattcagccacctacctctgtgccgttacaactgac agctgggggaaattgcagtttggagcagggacccaggttgtggtcaccccagatatc cagaaccctgaccctgccgtgtaccagctgagagactctaaatccagtgacaagtct gtctgcctattcaccgattttgattctcaaacaaatgtgtcacaaagtaaggattct gatgtgtatatcacagacaaatgtgtgctagacatgaggtctatggacttcaagagc aacagtgctgtggcctggagcaacaaatctgactttgcatgtgcaaacgccttcaac aacagcattattccagaagacaccttcttccccagcccagaaagttcctaagtcgac ggaggcggtgggggtagaatcgcccggctggaggaaaaagtgaaaaccttgaaagct cagaactcggagctggcgtccacggccaacatgctcagggaacaggtggcacagctt aaacagaaagtcatgaactactaggatcc

Figure 115

ggatccagcatggtgtctgaagctccctggaggctcctgcatgacagcgctgaca gtgacactgatggtgctgagctccccactggctttgtccggagacaccggagacacc ggaaacgctggtgtcactcagaccccaaaattccaggtcctgaagacaggacagagc atgacactgcagtgtgcccaggatatgaaccatgaatacatgtcctggtatcgacaa gacccaggcatggggctgaggctgattcattactcagttggtgctggtatcactgac caaggagaagtccccaatggctacaatgtctccagatcaaccacagaggatttcccg ctcaggctgctgctgctccctcccagacatctgtgtacttctgtgccagcagg ccgggactagcgggagggcgaccagagcagtacttcgggccgggcaccaggctcacg gtcacagaggacctgaaaaacgtgttcccacccgaggtcgctgtgtttgagccatca gaagcagagatctcccacacccaaaaggccacactggtgtgcctggccacaggcttc taccccgaccacgtggagctgagctggtgggtgaatgggaaggaggtgcacagtggg gtctgcacagacccgcagccctcaaggagcagcccgccctcaatgactccagatac gctctgagcagccgcctgagggtctcggccaccttctggcaggacccccgcaaccac ttccgctgtcaagtccagttctacgggctctcggagaatgacgagtggacccaggat agggccaaacccgtcacccagatcgtcagcgccgaggcctggggtagagcagactaa gtcgacggaggcggtgggggtagaatcgcccggctggaggaaaaagtgaaaaccttg aaagctcagaactcggagctggcgtccacggccaacatgctcagggaacaggtggca cagcttaaacagaaagtcatgaactactaggatcc

Figure 116

